

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/647, 072 A
Source: JFWO
Date Processed by STIC: 03/10/2006

ENTERED



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/647,072A

DATE: 03/10/2006

TIME: 15:31:45

Input Set : E:\substi SEQLIST 7853-267.TXT
 Output Set: N:\CRF4\03092006\J647072A.raw

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4 <110> APPLICANT: Kroczek, Richard
6 <120> TITLE OF INVENTION: COSTIMULATING POLYPEPTIDE OF T CELLS,
7 MONOCLONAL ANTIBODIES, AND THE PREPARATION AND USE THEREOF
10 <130> FILE REFERENCE: 7853-267-999
12 <140> CURRENT APPLICATION NUMBER: 10/647,072A
13 <141> CURRENT FILING DATE: 2003-08-22
15 <150> PRIOR APPLICATION NUMBER: 09/509,283
16 <151> PRIOR FILING DATE: 2000-08-11
18 <150> PRIOR APPLICATION NUMBER: PCT/DE98/02896
19 <151> PRIOR FILING DATE: 1998-09-23
21 <150> PRIOR APPLICATION NUMBER: DE 19821060.4
22 <151> PRIOR FILING DATE: 1998-05-11
24 <150> PRIOR APPLICATION NUMBER: DE 19741929.1
25 <151> PRIOR FILING DATE: 1997-09-23
27 <160> NUMBER OF SEQ ID NOS: 7
29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 2641
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (68) ... (667)
40 <220> FEATURE:
41 <223> OTHER INFORMATION: 8F4 DNA sequence
43 <400> SEQUENCE: 1
44 cgagaggctg aattcactgt cagcttgaa cactgaacgc gaggactgtt aactgtttct 60
45 ggcaaac atg aag tca ggc ctc tgg tat ttc ttt ctc ttc tgc ttg cgc 109
46 Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg
47 1 5 10
49 att aaa gtt tta aca gga gaa atc aat ggt tct gcc aat tat gag atg 157
50 Ile Lys Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met
51 15 20 25 30
53 ttt ata ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac 205
54 Phe Ile Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp
55 35 40 45
57 att gtc cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc 253
58 Ile Val Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu
59 50 55 60
61 tgc gat ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag 301
62 Cys Asp Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys
63 65 70 75
65 agt ctg aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt 349

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66	Ser	Leu	Lys	Phe	Cys	His	Ser	Gln	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	
67	80						85				90						
69	ttt	cta	tac	aac	ttg	gac	cat	tct	cat	gcc	aac	tat	tac	ttc	tgc	aac	397
70	Phe	Leu	Tyr	Asn	Leu	Asp	His	Ser	His	Ala	Asn	Tyr	Tyr	Phe	Cys	Asn	
71	95						100				105					110	
73	cta	tca	att	ttt	gat	cct	cct	ttt	aaa	gta	act	ctt	aca	gga	gga		445
74	Leu	Ser	Ile	Phe	Asp	Pro	Pro	Phe	Lys	Val	Thr	Leu	Thr	Gly	Gly		
75							115			120					125		
77	tat	ttg	cat	att	tat	gaa	tca	caa	ctt	tgt	tgc	cag	ctg	aag	ttc	tgg	493
78	Tyr	Leu	His	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Phe	Trp	
79							130			135					140		
81	tta	ccc	ata	gga	tgt	gca	gcc	ttt	gtt	gta	gtc	tgc	att	ttg	gga	tgc	541
82	Leu	Pro	Ile	Gly	Cys	Ala	Ala	Phe	Val	Val	Val	Cys	Ile	Leu	Gly	Cys	
83							145			150					155		
85	ata	ctt	att	tgt	tgg	ctt	aca	aaa	aag	aag	tat	tca	tcc	agt	gtg	cac	589
86	Ile	Leu	Ile	Cys	Trp	Leu	Thr	Lys	Lys	Tyr	Ser	Ser	Ser	Val	His		
87							160			165					170		
89	gac	cct	aac	ggt	gaa	tac	atg	ttc	atg	aga	gca	gtg	aac	aca	gcc	aaa	637
90	Asp	Pro	Asn	Gly	Glu	Tyr	Met	Phe	Met	Arg	Ala	Val	Asn	Thr	Ala	Lys	
91	175						180			185					190		
93	aaa	tct	aga	ctc	aca	gat	gtg	acc	cta	taa	tatggaactc	tggcacccag					687
94	Lys	Ser	Arg	Leu	Thr	Asp	Val	Thr	Leu	*							
95							195										
97	gcatgaagca	cggtggccag	ttttcctcaa	cttgaagtgc	aagattctct	tat	ttccggg										747
98	accacggaga	gtctgactta	actacataca	tcttcgtcgt	gtgtttgtt	caatctggaa											807
99	gaatgactgt	atcgtcaat	ggggatttta	acagactgcc	ttggtaactgc	cgagtccct											867
100	caaaacaaac	acccttgc	aaccagctt	ggagaaagcc	cagctctgt	gtgctcactg											927
101	ggagtggaat	ccctgtctcc	acatctgctc	ctagcagtgc	atcagccagt	aaaacaaaca											987
102	catttacaag	aaaaatgttt	taaagatgcc	aggggtactg	aatctgc当地	gcaaatgagc											1047
103	agccaaggac	cagcatctgt	ccgcatttca	ctatcatact	acctcttctt	tctgttaggaa											1107
104	tgagaattcc	tcttttaatc	agtcaaggga	gatgcttcaa	agctggagct	attttatttc											1167
105	tgagatgtt	atgtgaactg	tacattagta	catactcagt	actctccttc	aattgctgaa											1227
106	ccccagttga	ccattttacc	aagactttag	atgcttctt	gtgcctcaa	ttttcttttt											1287
107	aaaaataactt	ctacatgact	gcttgacagc	ccaaacagcc	ctctcaatag	agagctatgt											1347
108	cttacattct	ttcctctgct	gctcaatagt	tttatatact	tatgcataca	tatatacaca											1407
109	catatgtata	taaaattcat	aatgaatata	tttgcctata	ttctccctac	aagaatattt											1467
110	ttgctccaga	aagacatgtt	ctttctcaa	attcagttaa	aatggttac	tttgttcaag											1527
111	ttagtggtag	gaaacattgc	ccggaattga	aagcaaattt	attttattat	cctattttct											1587
112	accattatct	atgtttcat	ggtgctatta	attacaagtt	tagttcttt	tgttagatcat											1647
113	attaaaattg	caaacaaaat	catcttaat	gggccagcat	tctcatgggg	tagagcagaa											1707
114	tattcattta	gcctgaaagc	tgcagttact	ataggttgc	gtcagactat	acccatggtg											1767
115	cctctggct	tgacaggctca	aaatggtccc	catcagcctg	gagcagccct	ccagacctgg											1827
116	gtggattcc	agggttgaga	gactccccctg	agccagaggc	cacttaggtat	tcttgcctcc											1887
117	agaggctgaa	gtcacccctgg	gaatcacagt	ggtctacctg	cattcataat	tccaggatct											1947
118	gtgaagagca	catatgtgtc	agggcacaat	tccctctcat	aaaaaccaca	cagcctggaa											2007
119	attggccctg	gcccttcaag	atagccttct	ttagaatatg	atttggctag	aaagattctt											2067
120	aaatatgtgg	aatatgatta	ttcttagctg	gaatattttc	tctacttcct	gtctgcatac											2127
121	ccaaggcttc	tgaaggcagcc	aatgtcgatg	caacaacatt	tgtacttta	ggtaaactgg											2187
122	gattatgttg	tagttaaca	ttttgtaact	gtgtgcttat	agtttacaag	tgagacccga											2247

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123 tatgtcatta tgcatactta tattatctta agcatgtgta atgctggatg tgtacagtac 2307
124 agtactgaac ttgttaatttgc aatctagttt ggtgttctgt tttcagctga cttggacaac 2367
125 ctgactggct ttgcacaggt gttcccttag tttttgcag gtttctgtgt gtgggggtggg 2427
126 gtagtggggag gagaaccttc atggtgccc acctggcctg gttgtccaag ctgtgcctcg 2487
127 acacatcctc atccccagca tggacaccc caagatgaat aataattcac aaaatttctg 2547
128 tggaaatcaa tccagttta agaggagcca cttatcaaag agatttaac agtagtaaga 2607
129 agggaaagaa taaacatttgc atattcagca actg 2641
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 199
133 <212> TYPE: PRT
134 <213> ORGANISM: Homo sapiens
136 <400> SEQUENCE: 2
137 Met Lys Ser Gly Leu Trp Tyr Phe Phe Cys Leu Arg Ile Lys
138 1 5 10 15
139 Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
140 20 25 30
141 Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
142 35 40 45
143 Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
144 50 55 60
145 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
146 65 70 75 80
147 Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
148 85 90 95
149 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
150 100 105 110
151 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
152 115 120 125
153 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
154 130 135 140
155 Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
156 145 150 155 160
157 Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
158 165 170 175
159 Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
160 180 185 190
161 Arg Leu Thr Asp Val Thr Leu
162 195
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 17
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: Degenerate oligonucleotide
173 <220> FEATURE:
174 <221> NAME/KEY: misc_feature
175 <222> LOCATION: 3, 9, 15
176 <223> OTHER INFORMATION: n = A,T,C or G
178 <400> SEQUENCE: 3

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Input Set : E:\substi SEQLIST 7853-267.TXT
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W--> 179 mgnctsacng aygttnac	17
181 <210> SEQ ID NO: 4	
182 <211> LENGTH: 17	
183 <212> TYPE: DNA	
184 <213> ORGANISM: Artificial Sequence	
186 <220> FEATURE:	
187 <223> OTHER INFORMATION: Degenerate oligonucleotide	
189 <220> FEATURE:	
190 <221> NAME/KEY: misc_feature	
191 <222> LOCATION: 3, 9, 15	
192 <223> OTHER INFORMATION: n = A,T,C or G	
194 <400> SEQUENCE: 4	
W--> 195 mgnytdacng aygttnac	17
197 <210> SEQ ID NO: 5	
198 <211> LENGTH: 7	
199 <212> TYPE: PRT	
200 <213> ORGANISM: Homo sapiens	
202 <220> FEATURE:	
203 <223> OTHER INFORMATION: peptide found in 8F4-29 kDa sample	
205 <220> FEATURE:	
206 <221> NAME/KEY: VARIANT	
207 <222> LOCATION: 1	
208 <223> OTHER INFORMATION: Xaa = Any Amino Acid	
210 <400> SEQUENCE: 5	
W--> 211 Xaa Arg Leu Thr Asp Val Thr	
212 1 5	
215 <210> SEQ ID NO: 6	
216 <211> LENGTH: 6	
217 <212> TYPE: PRT	
218 <213> ORGANISM: Homo sapiens	
220 <400> SEQUENCE: 6	
221 Phe Asp Pro Pro Pro Phe	
222 1 5	
225 <210> SEQ ID NO: 7	
226 <211> LENGTH: 4	
227 <212> TYPE: PRT	
228 <213> ORGANISM: Homo sapiens	
230 <400> SEQUENCE: 7	
231 Tyr Met Phe Met	
232 1	

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/10/2006
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the

<220>

to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 3, 9, /15

Seq#:4; N Pos. 3, 9, /15

Seq#:5; Xaa Pos. 1

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Input Set : E:\substi SEQLIST 7853-267.TXT
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L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0